

## SUMMARIES

Result	Query	Match	Length	ID	Description
No.	Score		DB		
1	1638	100.0	1661	20	AAH6315
2	1620.2	98.9	1635	24	ABN6150
3	1613.4	86.3	2683	22	AAH5681
4	1140.4	69.6	1306	22	AAH5682
5	1122.6	68.5	1305	22	AAH5685
6	1062.4	64.9	1620	24	ABN6919
7	1062.4	64.9	2155561	24	ABN71327
8	1039.2	63.4	1623	22	AAH0800
9	1038.4	63.4	1926	22	AAH23036

10	1038	63.4	1654	20	AAH86153	DNA encoding a Str
11	1036	63.2	1647	22	AAH90906	zCFE 104 coding se
12	1036	63.2	2107	22	AAH56860	Antibiotic resistat
13	1034.4	63.2	5365	19	AAH52210	Streptococcus pneu
14	1029.6	62.9	2401	22	AAH56859	S. pneumoniae gfoE
15	954.2	58.3	2365589	24	ABH00551	Genomic sequence
16	942.6	57.5	3625	20	AAH12978	Enterococcus faeca
17	831.2	50.7	1901	20	ABH70705	Listeria monocyoc
18	823.2	50.3	213251	24	ABH67193	Listeria innocua c
19	785.4	47.5	1937	22	AAH56868	Listeria monocyoc
20	772	47.1	1936	22	AAH56867	S. aureus RM42020
21	750.0	46.4	1570	24	ABH65121	Methicillin resist
22	755.4	46.1	1620	20	AAH56598	Listeria monocyoc
23	755.4	46.1	3885	22	AAH55519	S. epidermidis ope
24	734.6	44.8	1633	24	AAH924405	S. epidermidis gen
25	721.4	44.0	2712	22	AAH56866	Staphylococcus epi
26	704.2	43.0	1647	18	AAH656201	S. aureus gfoE ope
27	674.2	39.9	9472	18	AAH656203	Lawsonia intracell
28	654.2	39.9	96109	22	AAH28548	Genomic fragment #
29	615.8	37.6	640681	24	AAH92787	Buchnera sp. genom
30	608.2	37.1	613	22	AAH56864	Antibiotic resistat
31	604.2	36.9	609	22	AAH56863	E. coli groEL codi
32	589.8	36.0	1647	21	AAH44498	Escherichia coli G
33	589.8	36.0	1647	22	AAH90805	Escherichia coli G
34	589.8	36.0	1647	22	ABH96324	Nucleotide sequenc
35	589.8	36.0	1741	22	AAH58456	E. coli K12 strain
36	589.8	36.0	2155	24	AAH34423	E. coli groSL gen
37	589.8	36.0	4524	21	AAH45500	Escherichia coli g
38	587.6	35.9	1655	20	AAH86152	DNA encoding a Str
39	577.2	35.6	2032	22	AAH86152	Multidrug resistan
40	577.2	35.6	2006	22	AAH86152	Droptahogen E. coli
41	555.2	33.2	1662	22	AAH36857	DNA encoding a Str
42	552.8	33.7	1635	21	AAH25509	Neisseria meningit
43	550	33.6	2465	12	AAH10328	Hyp operon. Chlam
44	549.8	32.6	910715	20	AAH10328	Neisseria burgordei
45	536.8	31.8	1635	21	AAH13000	Neisseria meningit

## ALIGNMENTS

	RESULT 1
AAx86155	
ID	AAx86155 standard; DNA; 1661 BP.
AC	AAx86155;
DT	22-SEP-1999 (first entry)
DE	DNA encoding a Streptococcus pyogenes heat shock protein (Hsp)60-2.
XX	
KM	Heat shock protein; Hsp60-2; immune response; immunological carrier
KW	cancer control; tumour; sarcoma; cancer; gene therapy; ss.
OS	Streptococcus pyogenes.
PN	WO9935270-A1.
PD	15-JUL-1999.
PF	29-DEC-1998; 98MO-CAN01203.
PR	31-DEC-1997; 97US-0001737.
PA	(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
PI	Mizzen L, Misilewski J;
PP	WPI; 1999-430397/36.
DR	P-PsDB; AAY23904.
PT	New nucleic acid encoding heat shock protein-60 from Streptococcus,
XX	useful in vaccines, as carriers for other immunogens, as anticancer

PT agents and for diagnosis  
XX  
PS Claim 3, Fig 4A-B; 176pp; English.  
XX  
The present sequence encodes a heat shock protein, designated Hsp60-2.  
CC The protein, its fragments, variants and fusion proteins, are  
CC used to elicit or enhance an immune response against Streptococcus,  
CC and to elicit a similar response to a target antigen fused to the  
CC protein. Unlike other immunological carriers, Hsp60 proteins are not  
CC immunosuppressive so provide an increased response to any conjugated or  
CC fused antigen. Also, where used for cancer control, they lack the side  
CC effects associated with endotoxins. They can also be used to detect  
CC specific antibodies and in treatment or prevention of tumours  
CC (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or  
CC liver). The Hsp60 polynucleotide is used for recombinant production  
CC of the protein, as a source of primers and probes for detecting  
CC streptococci in standard hybridization/amplification assays, and  
CC therapeutically in gene therapy vectors.  
XX  
SQ Sequence 1661 BP; 512 A; 308 C; 407 G; 434 T; 0 other;

Query Match 100.0%; Score 1638; DB 20; Length 1661;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGAAGAAATCAATTTTCAGCAGATGCGCTGCTGCATGGTGGCGAGTTGAT 60  
DB 15 ATGCGAAGAAATCAATTTTCAGCAGATGCGCTGCTGCATGGTGGCGAGTTGAT 74  
QY 61 ATGTAGCAGATACGCTCAAGTAAAGCTGCTAAAGGGGCAATGTTGTTCTGAA 120  
DB 75 ATGTAGCAGATACGCTCAAGTAAAGCTGCTAAAGGGGCAATGTTGTTCTGAA 134  
QY 121 AAAGCTTTGGTCTCCCTTAATTAATGAGCGGGGAAACATTCCTTAAGAAATGAA 180  
DB 135 AAAGCTTTGGTCTCCCTTAATTAATGAGCGGGGAAACATTCCTTAAGAAATGAA 194  
QY 181 TTAGAAGTCAATTTTAAACATGGAGCAAAATTTGTCGTAAGTGGCTTTAAACC 240  
DB 195 TTAGAAGTCAATTTTAAACATGGAGCAAAATTTGTCGTAAGTGGCTTTAAACC 254  
QY 241 AATGATATCTGCTGATGGAGCAGTACTGCAACAGTTTGAACAGCCATTGTCAT 300  
DB 255 AATGATATCTGCTGATGGAGCAGTACTGCAACAGTTTGAACAGCCATTGTCAT 314  
QY 301 GAAGACTAAAAAATGTGACAGAGTGTCTAATCCATGTTGCTCGTGAGGATTGAA 360  
DB 315 GAAGACTAAAAAATGTGACAGAGTGTCTAATCCATGTTGCTCGTGAGGATTGAA 374  
QY 361 ACAGCAACAGCAACAGCTGTTGAAGCCTTGAAGCAATGCTCAACCTGTTCTGCAAG 420  
DB 375 ACAGCAACAGCAACAGCTGTTGAAGCCTTGAAGCAATGCTCAACCTGTTCTGCAAG 434  
QY 421 GAAGCTATGCTAGTGTGCTGAGTATCATAGCTCTGAAAGAGTTGAGAGATTATC 480  
DB 435 GAAGCTATGCTAGTGTGCTGAGTATCATAGCTCTGAAAGAGTTGAGAGATTATC 494  
QY 481 TCAGAACTATGAGCGTGTGGCAACAGTGTGTATTCACATGCAAGAAATTCAGAGT 540  
DB 495 TCAGAACTATGAGCGTGTGGCAACAGTGTGTATTCACATGCAAGAAATTCAGAGT 554  
QY 541 ATGGAACAGCACTGAAGTGTGAAGGCATGCAATTTGACCCGTGTTACCTGTCGA 600  
DB 555 ATGGAACAGCACTGAAGTGTGAAGGCATGCAATTTGACCCGTGTTACCTGTCGA 614  
QY 601 TACATGCTCAGACACATGAATAATGTTGACAGCTTGAAACCCATTATCTTATTC 660  
DB 615 TACATGCTCAGACACATGAATAATGTTGACAGCTTGAAACCCATTATCTTATTC 674  
QY 661 ACGGATAAAAAAGTGTCAACATCAAGACATTTTGGCATCTAGTATGAGAGTTCTTAA 720  
DB 675 ACGGATAAAAAAGTGTCAACATCAAGACATTTTGGCATCTAGTATGAGAGTTCTTAA 734

QY 721 ACACAGCTGCATCTATCTATTTGAGAGTATGATGATGAGCACTTCACACCTT 780  
DB 735 ACACAGCTGCATCTATCTATTTGAGAGTATGATGATGAGCACTTCACACCTT 794  
QY 781 GTCTTGAACAAATTCGTTGCTACTTTCAATGCTGTCTGCAAGCCAGGATTTGTT 840  
DB 795 GTCTTGAACAAATTCGTTGCTACTTTCAATGCTGTCTGCAAGCCAGGATTTGTT 854  
QY 841 GATCTGTGAAGCTATGCTTGAAGCAATTCATCTTACACAGTGTGATGATTTACA 900  
DB 855 GATCTGTGAAGCTATGCTTGAAGCAATTCATCTTACACAGTGTGATGATTTACA 914  
QY 901 GAGGATCTAGGACTTGAATTTAAAGATGCTACATGACAGCCCTTGAGAGCTGCTAAG 960  
DB 915 GAGGATCTAGGACTTGAATTTAAAGATGCTACATGACAGCCCTTGAGAGCTGCTAAG 974  
QY 961 ATTACAGTTGATAAAGATAGCAGATTAATGTTGAAGGTTGAGAGGATTCAGAGCTATT 1020  
DB 975 ATTACAGTTGATAAAGATAGCAGATTAATGTTGAAGGTTGAGAGGATTCAGAGCTATT 1034  
QY 1021 GCTACGCTATTCGACGCTGATTAATGCAATTTGAAGCAACACTTGTGATGACCGT 1080  
DB 1035 GCTACGCTATTCGACGCTGATTAATGCAATTTGAAGCAACACTTGTGATGACCGT 1094  
QY 1081 GAAACCTCAAGAACTGTTGGGCAAAATTAAGTGTGTGCTGTATCAABATAGA 1140  
DB 1095 GAAACCTCAAGAACTGTTGGGCAAAATTAAGTGTGTGCTGTATCAABATAGA 1154  
QY 1141 GCTCCACAGAGACGCTTTAAAGAAATGAACCTTGCAATGAGATGCTTAATGCT 1200  
DB 1155 GCTCCACAGAGACGCTTTAAAGAAATGAACCTTGCAATGAGATGCTTAATGCT 1214  
QY 1201 ACAGCTGACCGCTTGAAGAGTATCGTGTGTGTGAGACAGCACTTATACGTT 1260  
DB 1215 ACAGCTGACCGCTTGAAGAGTATCGTGTGTGTGAGACAGCACTTATACGTT 1274  
QY 1261 ATTGAAGAAAGTACAGCTCTTGAAGGAGATGATGATGAGAGTAACTTGTG 1320  
DB 1275 ATTGAAGAAAGTACAGCTCTTGAAGGAGATGATGATGAGAGTAACTTGTG 1334  
QY 1321 CTTCGTGCTCTAGAAAGCCCTGACGTCATTAATGCTGAGTGAAGAGGCTGC 1380  
DB 1335 CTTCGTGCTCTAGAAAGCCCTGACGTCATTAATGCTGAGTGAAGAGGCTGC 1394  
QY 1381 GTAGTATGACAGCTGTAAGAAACAGCCCTGACAGAAAGATTTAATGCTGCAACAGT 1440  
DB 1395 GTAGTATGACAGCTGTAAGAAACAGCCCTGACAGAAAGATTTAATGCTGCAACAGT 1454  
QY 1441 GATGGGTTGATATGATTTAAACAGGAATCAATGACCTGTCAAAGTAACAGATCAGCG 1500  
DB 1455 GATGGGTTGATATGATTTAAACAGGAATCAATGACCTGTCAAAGTAACAGATCAGCG 1514  
QY 1501 CTTCAAATGACGCTTGTGATAGTCTTATTTTGAACAGAGCAAGTGTGCTAAT 1560  
DB 1515 CTTCAAATGACGCTTGTGATAGTCTTATTTTGAACAGAGCAAGTGTGCTAAT 1574  
QY 1561 AAACCTGAACAGCTACAGCCAGCCAGCAATGCCAGAGTATGATCAGAGATGATG 1620  
DB 1575 AAACCTGAACAGCTACAGCCAGCCAGCAATGCCAGAGTATGATCAGAGATGATG 1634  
QY 1621 GGTGGATGGGCGGATTA 1638  
DB 1635 GGTGGATGGGCGGATTA 1652

RESULT 2  
ABN69160 standard; DNA: 1635 BP.  
XX  
XX ABN69160:  
XX  
XX 01-JUL-2002 (first entry)  
XX

DE Streptococcus polynucleotide SEQ ID NO 6233.  
 XX Streptococcus: GAS; GAS: group B streptococcus; Streptococcus agalactiae;  
 KM group A streptococcus; Streptococcus pyogenes; antibacterial; gene;  
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.  
 OS Streptococcus pyogenes.  
 PN WO200234771-A2.  
 PD 02-MAY-2002.  
 PF 29-OCT-2001; 2001WO-GB04789.  
 PR 27-OCT-2000; 2000GB-0026333.  
 PR 24-NOV-2000; 2000GB-0028727.  
 PR 07-MAR-2001; 2001GB-0005640.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX Telford J, Maignani V, Margalit Ros YI, Grandi G, Fraser C.  
 PI Tettelin H;  
 DR WPI: 2002-352536/38.  
 DR P-PSDB: ABP28529.  
 XX New Streptococcus protein for the treatment or prevention of infection  
 PT or disease caused by Streptococcus bacteria, such as meningitis, and  
 PT for detecting a compound that binds to the protein -  
 PS Claim 7; Page 3785-3786; 4525pp: English.  
 CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and  
 CC antibodies that bind (1) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a  
 CC biological sample. (1) is used to determine whether a compound binds to  
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (1) may be used to recombinantly produce (1) and may be  
 CC used in gene therapy. Antibodies to (1) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins.  
 XX Sequence 1635 BP; 504 A; 303 C; 397 G; 431 T; 0 other;  
 SQ  
 Query Match 98.9%; Score 1620.2; DB 24; Length 1635;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1622; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 241 AATGATATGCTGTGATAGGACGACACTGACACAGTTTGGACACAGCCATTGTCAT 300  
 DB 247 AATGATATGCTGTGATAGGACGACACTGACACAGTTTGGACACAGCCATTGTCAT 306  
 QY 301 GAAGACATTAATAATGTGACAGCAGGTGTAATCCAAATTTGGTATCCGTGAGGATGAA 360  
 DB 307 GAAGACATTAATAATGTGACAGCAGGTGTAATCCAAATTTGGTATCCGTGAGGATGAA 366  
 QY 361 ACAGCAACGACACAGCTTGTGAAGCCTTGAAGCCATTGCTCAACCTGTATCTGGCAG 420  
 DB 367 ACAGCAACGACACAGCTTGTGAAGCCTTGAAGCCATTGCTCAACCTGTATCTGGCAG 426  
 QY 421 GAAGCTATGCTCAGGTGCTGAGTATCATCAGCTCTGAAAAGTTGGAAGATATATC 480  
 DB 427 GAAGCTATGCTCAGGTGCTGAGTATCATCAGCTCTGAAAAGTTGGAAGATATATC 486  
 QY 481 TCAGAGGTATGAGAGGTGCTGAGCAGCAGTGTGATTAACATCCGAATATCTGAGGT 540  
 DB 487 TCAGAGGTATGAGAGGTGCTGAGCAGCAGTGTGATTAACATCCGAATATCTGAGGT 546  
 QY 541 ATGGAACACAGACTTAAGTGTGGAAGCAGTCAATTTGACCGTGTACCTGTCTCAA 600  
 DB 547 ATGGAACACAGACTTAAGTGTGGAAGCAGTCAATTTGACCGTGTACCTGTCTCAA 606  
 QY 601 TACATGTGACAGACATGATAAATAATGTTGACAGCTTGAATAACCATTTATCTATATC 660  
 DB 607 TACATGTGACAGACATGATAAATAATGTTGACAGCTTGAATAACCATTTATCTATATC 666  
 QY 661 ACAGATTAATAATGTGACAGCAGTCAATTTGACAGCTTGAATAACCATTTATCTATATC 720  
 DB 667 ACAGATTAATAATGTGACAGCAGTCAATTTGACAGCTTGAATAACCATTTATCTATATC 726  
 QY 721 ACCAAGCTCATCTACTATTTATGAGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 DB 727 ACCAAGCTCATCTACTATTTATGAGATGATGATGATGATGATGATGATGATGATGATGAT 786  
 QY 781 GCTTGACAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 DB 787 GCTTGACAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846  
 QY 841 GATGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 DB 847 GATGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906  
 QY 901 GAGATCTAGAGCTTGAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 DB 907 GAGATCTAGAGCTTGAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 966  
 QY 961 ATTACAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
 DB 967 ATTACAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026  
 QY 1021 GCTAACGATATGCTATGATTAATGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 1080  
 DB 1027 GCTAACGATATGCTATGATTAATGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 1086  
 QY 1081 GAAATACATGACAGCTTGAAGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 1140  
 DB 1087 GAAATACATGACAGCTTGAAGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 1146  
 QY 1141 GCTCAACAGACAGCTTGAAGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 1200  
 DB 1147 GCTCAACAGACAGCTTGAAGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 1206  
 QY 1201 ACAGCTGACAGCTTGAAGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 1260  
 DB 1207 ACAGCTGACAGCTTGAAGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 1266  
 QY 1261 ATTGAATAAGTACAGCTTGAAGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 1320  
 DB 1267 ATTGAATAAGTACAGCTTGAAGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 1326  
 QY 1321 CTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380

CC inhibiting expression of GL or GS in cells or tissues *in vitro*. (1) are  
CC also useful for inhibiting the growth of a microorganism, or inhibiting  
CC the expression of GL or GS gene in a microorganism (a bacterial cell or  
CC a virus) having a GL or GS gene which involves administering to the  
CC microorganism or to a cell infected with the microorganism, (1). (1) are  
CC also useful for treating a mammalian pathological condition mediated by  
CC the microorganisms which involves identifying a eukaryotic organism  
CC having a pathological condition mediated by microorganisms having a GL  
CC or GS gene and administering (1) such that the growth of microorganism  
CC is inhibited. The antisense compounds are utilized for diagnostics,  
CC therapeutics, prophylaxis and as research reagents and kits, e.g., to  
CC prevent or delay microbial infections in humans. They are also useful as  
CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854  
CC represent PCR primers for gene sequences which are used in the  
CC exemplification of the present invention. AAH56655 to AAH56870 represent  
CC gene nucleotide sequence given in the present invention.

XX  
XN  
SQ Sequence 2683 BP; 808 A; 490 C; 593 G; 792 T; 0 other;

Query Match 86.3%; Score 1413.4; DB 22; Length 2683;  
Best Local Similarity .98.9%; Pred No. 0;

56861 standard; DNA; 2683 BP.

56861;

SEP-2001 (first entry)

pyogenes groEL gene partial sequence SEQ ID NO:7

isense oligonucleotide; groE; groEL; groES; inhibitor; growth;

*Staphylococcus aureus*; *Pseudomonas aeruginosa*; *Streptococcus pyogenes*; *Staphylococcus aureus*; *Pseudomonas aeruginosa*.

Probiol Infection; ds.

**Streptococcus pyogenes.**

00136625-A2.

MAY - 2001.

NOV-2000; 2000WO-CA01347.

NOV-1999; 99US-0166249.

GENESENSE TECHNOLOGIES INC

ght JA, Young AH, Dugourd D;

2001-355633/37.

antibiotic compounds targeting nucleic acid encoding groEL or

pression of the genes, useful to inhibit growth of microorganism and the genes -

Closure: E1a 7: 110000: Enclosed

present invention accordingly, the present invention

oligonucleotides to nucleotide sequences encoding groE. More

targeted to a nucleotide sequence encoding groEL (heat

microorganism, where the antisense compound is complementary to GL or

pression of GL or GS, is claimed. (I) have antibacterial, antiviral and proliferative activities and can be used in combination with

for inhibition of expression of groES or groEL. (I) are useful for

Db 721 CTAGAGCTTGATTAAGATGCTACATGACAGCCCTGGACAGGCTGCTAAGATTACA 780  
 Qy 967 GTTGATTAAGATGACAGCTAATTTGTTGAGCTTCAGAAAGTTCAAGATTCCTTAC 1026  
 Db 781 GTTGATTAAGATGACAGCTAATTTGTTGAGCTTCAGAAAGTTCAAGATTCCTTAC 840  
 Qy 1027 GCTATGCTAGCTAATTAATTCGAAATTAAGAACACAACTTCTGACTTGCAGGAAAA 1086  
 Db 841 GCGATCTCAGCTAATTAATTCGAAATTAAGAACACAACTTCTGACTTGCAGGAAAA 900  
 Qy 1087 CTACAGAACCTTGGCGAATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1146  
 Db 901 CTACAGAACCTTGGCGAATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960  
 Qy 1147 ACAGAGACAGCTTAAAGAAATGAAGAACTGGCAATGAGATGCTTAATGCTACAGT 1206  
 Db 961 ACAGAGACAGCTTAAAGAAATGAAGAACTGGCAATGAGATGCTTAATGCTACAGT 1020  
 Qy 1207 GCAGCGCTGAGAGAGTATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1266  
 Db 1021 GCAGCGCTGAGAGAGTATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1080  
 Qy 1267 AAATGACAGCTTGTGAGCTTGAAGGCGATGATCTACTGAGCTAACATTGTGCTTGT 1326  
 Db 1081 AAATGACAGCTTGTGAGCTTGAAGGCGATGATCTACTGAGCTAACATTGTGCTTGT 1140  
 Qy 1327 GCTCTAGAGAGCTGTAGCTCAAAATTCCTTAAATGCTGGTACGAAAGGCTCCGACTT 1386  
 Db 1141 GCTCTAGAGAGCTGTAGCTCAAAATTCCTTAAATGCTGGTACGAAAGGCTCCGACTT 1200  
 Qy 1387 ATTGACAACTTGAAGAAACAGCCCTGAGAGACAGATTAATGCTGCAAGAGTATGG 1446  
 Db 1201 ATTGACAACTTGAAGAAACAGCCCTGAGAGACAGATTAATGCTGCAAGAGTATGG 1260  
 Qy 1447 GTTGATATGATTAAGAAACAGATTAATGCTGCAAGAGTATGGTATGCTTAA 1506  
 Db 1261 GTTGATATGATTAAGAAACAGATTAATGCTGCAAGAGTATGGTATGCTTAA 1320  
 Qy 1507 AATGCAAGCTTGTGAGCTTATCTTATTTGACAGAGAAAGCAAGTGTGCTTAATAACT 1566  
 Db 1321 AATGCAAGCTTGTGAGCTTATCTTATTTGACAGAGAAAGCAAGTGTGCTTAATAACT 1380  
 Qy 1567 GAACGACAGCTGAGCGGACGACCAATGCGACAGAGTATGATCCAGAAATGATGGGTG 1625  
 Db 1381 GAACGACAGCTGAGCGGACGACCAATGCGACAGAGTATGATCCAGAAATGATGGGTG 1439

RESULT 4  
 AAH56862  
 ID AAH56862 standard; DNA; 1306 BP.  
 AC AAH56862;  
 DT 06-SEP-2001 (first entry)  
 DE  
 XX Antibiotic resistant *S. pyogenes* groEL gene partial sequence SEQ ID:8.  
 KW Antisense oligonucleotide; groEL; groEL; groEL; inhibitor; growth;  
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;  
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;  
 KW antibacterial; antiviral; antiproliferative; antisense therapy;  
 KW microbial infection; ds.  
 OS Streptococcus pyogenes.  
 XX  
 XX  
 XX NO200136625-A2.  
 XX  
 XX 25-MAY-2001.  
 XX  
 XX 20-NOV-2000; 2000WO-CA01347.  
 XX  
 XX 18-NOV-1999; 99US-0166249.  
 XX

PA (GENE-) GENESENSE TECHNOLOGIES INC.  
 XX Wright JA, Young AH, Dugourd D;  
 PI WPI; 2001-355633/37.  
 DR  
 XX Novel antisense compounds targeting nucleic acid encoding groEL or  
 PT groEL gene of microorganism, which hybridize with and inhibit  
 PT expression of the genes, useful to inhibit growth of microorganism  
 XX having the genes.  
 XX  
 PS Disclosure: Fig 8; 110pp; English.  
 XX  
 CC The present invention specifically claims AAH56368 to AAH56832 which are  
 CC antisense oligonucleotides to nucleotide sequences encoding groEL. More  
 CC generally, antisense compounds (I) comprising antisense oligonucleotides  
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat  
 CC shock protein (HSP160) (GL) and groES (HSP10) (GS) gene from a  
 CC microorganism, where the antisense compound is complementary to GL or  
 CC GS of a microorganism and specifically hybridizes with and inhibits the  
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral  
 CC and antiproliferative activities, and can be used in antisense therapy  
 CC for inhibiting expression of groES or groEL. (I) are useful for  
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are  
 CC also useful for inhibiting the growth of a microorganism, or inhibiting  
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or  
 CC a virus) having a GL or GS gene which involves administering to the  
 CC microorganism or to a cell infected with the microorganism. (I) are  
 CC also useful for treating a mammalian pathological condition mediated by  
 CC the microorganism which involves identifying a microorganism having a GL  
 CC or GS gene and administering (I) such that the growth of microorganism  
 CC is inhibited. The antisense compounds are utilized for diagnostics,  
 CC therapeutics, prophylaxis and as research reagents and kits, e.g. to  
 CC prevent or delay microbial infections in humans. They are also useful as  
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56832 to AAH56854  
 CC represent PCR primers for groE sequences which are used in the  
 CC exemplification of the present invention. AAH56855 to AAH56870 represent  
 CC groE nucleotide sequence given in the present invention.  
 XX  
 XX  
 SO Sequence 1306 BP; 407 A; 235 C; 308 G; 356 T; 0 other;  
 Query Match 69.6%; Score 1140.4; DB 22; Length 1306;  
 Best Local Similarity: 99.9%; Pred. No. 1,96-286;  
 Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 484 GAACCTGAGAGCTGTGGCAAGATGCTGTATACCATGAAGATTCGAGGTAG 543  
 Db 2 GAACCTGAGAGCTGTGGCAAGATGCTGTATACCATGAAGATTCGAGGTAG 61  
 Qy 544 GAACGAGAACTGGAAGTGGTGAAGGACATGCAATTGACCGTGTACCTCAATAC 603  
 Db 62 GAACGAGAACTGGAAGTGGTGAAGGACATGCAATTGACCGTGTACCTCAATAC 121  
 Qy 604 ATGCTCAGACAAATGAAAAATGTTGTCAGACCTGAAACCCCTTAATCTAATCAG 663  
 Db 122 ATGCTCAGACAAATGAAAAATGTTGTCAGACCTGAAACCCCTTAATCTAATCAG 181  
 Qy 664 GATTAAGAAAGTCAACCAACCAAGCAATTTGGCACTCTTGAGAGATCTTAAAC 723  
 Db 182 GATTAAGAAAGTCAACCAACCAAGCAATTTGGCACTCTTGAGAGATCTTAAAC 241  
 Qy 724 AACCTCCATTCATTCATTCATGATGATGATGATGATGATGATGATGATGATGATG 783  
 Db 242 AACCTCCATTCATTCATTCATGATGATGATGATGATGATGATGATGATGATGATG 301  
 Qy 784 TTGACAGAGTTCGTGTACTTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 843  
 Db 302 TTGACAGAGTTCGTGTACTTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 361  
 Qy 844 CGTGTAAAGCTATGTTGAAGACATTTGCTATCTTGAAGGTGTGTACATGATTAAGAG 903  
 Db 362 CGTGTAAAGCTATGTTGAAGACATTTGCTATCTTGAAGGTGTGTACATGATTAAGAG 421

OY 904 GATCTAGAGCTTGAATTAAAGATGCTACATGACAGCCCTTGACAGGCTGTAGAT 963  
 DB 422 GATCTAGAGCTTGAATTAAAGATGCTACATGACAGCCCTTGACAGGCTGTAGAT 481  
 OY 964 ACAGTTGATTAAGATACACAGATTAATTTGTAAGGTTGAGATTAAGATTAAGTCT 1023  
 DB 482 ACAGTTGATTAAGATACACAGATTAATTTGTAAGGTTGAGATTAAGATTAAGTCT 541  
 OY 1024 AACCTATGACATGATTAATTCGCAATTAAGTAAGCAACACTTCTGACTTGAACGTTAA 1083  
 DB 542 AACCTATGACATGATTAATTCGCAATTAAGTAAGCAACACTTCTGACTTGAACGTTAA 601  
 OY 1084 AACCTATGACATGATTAATTCGCAATTAAGTAAGCAACACTTCTGACTTGAACGTTAA 1143  
 DB 602 AACCTATGACATGATTAATTCGCAATTAAGTAAGCAACACTTCTGACTTGAACGTTAA 661  
 OY 1144 CGAAGAGACAGCTTTAAAGAAATGAAGAACTTGCATGATGAGATGCTTAATGCTTACA 1203  
 DB 662 CGAAGAGACAGCTTTAAAGAAATGAAGAACTTGCATGATGAGATGCTTAATGCTTACA 721  
 OY 1204 CGTGCAGCCGTTGAAAGAGATTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263  
 DB 722 CGTGCAGCCGTTGAAAGAGATTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781  
 OY 1264 GAAAAAGTAGACAGCTTGTAGCTTGTAGGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCT 1323  
 DB 782 GAAAAAGTAGACAGCTTGTAGCTTGTAGGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCT 841  
 OY 1324 CGTGCCTAGAGAGAGCTTGTAGCTTGTAGGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCT 1383  
 DB 842 CGTGCCTAGAGAGAGCTTGTAGCTTGTAGGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCT 901  
 OY 1384 GTTATTGACAGTTGAAAG 1443  
 DB 902 GTTATTGACAGTTGAAAG 961  
 OY 1444 TGGTGTATGATTAATTAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1503  
 DB 962 TGGTGTATGATTAATTAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1021  
 OY 1504 CAAATGACAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCT 1563  
 DB 1022 CAAATGACAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCTTGTAGCT 1081  
 OY 1564 CCTGAACAGCTAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGC 1623  
 DB 1082 CCTGAACAGCTAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGC 1623  
 OY 1624 GG 1625  
 DB 1142 GG 1143

RESULT 5  
 AAH5685  
 ID AAH5685 standard; DNA; 1305 BP.

XX AAH5685:  
 XX 06-SEP-2001 (first entry)  
 XX  
 XX Antibiotic resistant *S. pyogenes* groEL gene partial sequence SEQ ID:11.  
 XX  
 XX Antisense oligonucleotide; groEL; groEL; groEL; inhibitory; growth;  
 XX microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;  
 XX Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;  
 XX antibacterial; antiviral; antiproliferative; antisense therapy;  
 XX microbial infection; ds.  
 XX  
 XX Streptococcus pyogenes.  
 XX  
 XX PN: MO200136625-A2.

XX  
 PD 25-MAY-2001.  
 XX  
 PF 20-NOV-2000; 2000MO-CA01347.  
 XX  
 PR 18-NOV-1999; 9905-0166249.  
 XX  
 PA (GENE-) GENESENSE TECHNOLOGIES INC.  
 XX  
 PI Wright JA, Young AH, Dugourd D;  
 XX WPI: 2001-355633/37.  
 DR  
 XX  
 PT Novel antisense compounds targeting nucleic acid encoding groEL or  
 PT groEL gene of microorganism, which hybridize with and inhibit  
 PT expression of the genes, useful to inhibit growth of microorganism  
 PT having the genes.  
 XX  
 PS Disclosure; Fig 11; 110pp; English.  
 XX  
 CC The present invention specifically claims AAH56368 to AAH56372 which are  
 CC antisense oligonucleotides to nucleotide sequences encoding groEL. More  
 CC generally, antisense compounds (i) comprising antisense oligonucleotides  
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat  
 CC shock protein (HSP) 60) (GL) and groEL (HSP10) (GS) gene from a  
 CC microorganism, where the antisense compound is complementary to GL or  
 CC GS of a microorganism and specifically hybridizes with and inhibits the  
 CC expression of GL or GS, is claimed. (ii) have antibacterial, antiviral  
 CC and antiproliferative activities, and can be used in antisense therapy  
 CC and for inhibition of expression of GL or GS in cells or tissues *in vitro*. (i) are  
 CC also useful for inhibiting the growth of a microorganism, or inhibiting  
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or  
 CC a virus) having a GL or GS gene which involves administering to the  
 CC microorganism or to a cell infected with the microorganism, (i). (i) are  
 CC also useful for treating a mammalian pathological condition mediated by  
 CC the microorganisms which involves identifying a eukaryotic organism having a GL  
 CC or GS gene and administering (i) such that the growth of microorganism  
 CC is inhibited. The antisense compounds are utilized for diagnostics,  
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to  
 CC prevent or delay microbial infections in humans. They are also useful as  
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56373 to AAH56384  
 CC represent PCR primers for groEL sequences which are used in the  
 CC amplification of the present invention. AAH56855 to AAH56870 represent  
 CC groEL nucleotide sequence given in the present invention.  
 XX  
 XX Sequence 1305 BP; 406 A; 238 C; 312 G; 349 T; 0 other;  
 XX  
 XX Query Match 68.5%; Score 1122.6; DB 22; Length 1305;  
 XX Best Local Similarity 99.2%; Pred. No. 8.7e-284;  
 XX Matches 1128; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 OY 489 TATGAGAGCTGTGGGCAAGAGATGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 548  
 DB 1 TATGAGAGCTGTGGGCAAGAGATGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 60  
 OY 549 AGAAGTTGAAGTTGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 608  
 DB 61 AGAAGTTGAAGTTGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120  
 OY 609 CACAGACATTAATAAATGATGTCAGACCTTGAAGAAACCATTAATTAATTAATTAATTAATTAAT 668  
 DB 121 CACAGACATTAATAAATGATGTCAGACCTTGAAGAAACCATTAATTAATTAATTAATTAATTAAT 180  
 OY 669 AAAAGTTCAAACATCCCAAGACATTTTGCACACTTGTAGAGAGTTCTTAATAACCAACG 728  
 DB 181 AAAAGTTCAAACATCCCAAGACATTTTGCACACTTGTAGAGAGTTCTTAATAACCAACG 240  
 OY 729 TCCATTACTCATTAATTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 788  
 DB 241 TCCATTACTCATTAATTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300





361 ACAGCAACAGACAGCTGTTGAACCTTGAAGCCATGCTCAACCTGATCTGCGAAG 420  
 Db 361 ACAGCTGTTTCACAGCAGCTGTTGAAGCCATGCTCAACCTGATCTGCGAAG 420  
 421 GAAGCTATGCTCAGCAGCTGTTGAAGCCATGCTCAACCTGATCTGCGAAG 480  
 Db 421 GAAGCTATGCTCAGCAGCTGTTGAAGCCATGCTCAACCTGATCTGCGAAG 480  
 481 TCAGAACCTATGAGCAGCTGTTGAAGCCATGCTCAACCTGATCTGCGAAG 540  
 Db 481 TCAGAACCTATGAGCAGCTGTTGAAGCCATGCTCAACCTGATCTGCGAAG 540  
 541 ATGGAACAGAACTTGAAGCTGTTGAAGCCATGCTCAACCTGATCTGCGAAG 600  
 Db 541 ATGGAACAGAACTTGAAGCTGTTGAAGCCATGCTCAACCTGATCTGCGAAG 600  
 601 TACATGCTCAGACAAATGAAATGCTGAAACCTGAAACCTGATCTGCGAAG 660  
 Db 601 TACATGCTCAGACAAATGAAATGCTGAAACCTGAAACCTGATCTGCGAAG 660  
 661 ACGATTAAGAAAGTGTCAACATCCAGCACTTTGCACTGAGAGAGTCTTAA 720  
 Db 661 ACGATTAAGAAAGTGTCAACATCCAGCACTTTGCACTGAGAGAGTCTTAA 720  
 721 ACGAACCTGCTATCTCAATATTCAGAGATGCTGAGAGAGTCTTAA 780  
 Db 721 ACGAACCTGCTATCTCAATATTCAGAGATGCTGAGAGAGTCTTAA 780  
 781 GCTTGAACAGATCTGCTGATCTTCAATGCTGCTGCAAGCCAGAGATTTGT 840  
 Db 781 GCTTGAACAGATCTGCTGATCTTCAATGCTGCTGCAAGCCAGAGATTTGT 840  
 841 GATGCTGTAAGATCTGCTGATCTTCAATGCTGCTGCAAGCCAGAGATTTGT 900  
 Db 841 GATGCTGTAAGATCTGCTGATCTTCAATGCTGCTGCAAGCCAGAGATTTGT 900  
 901 GAGATCTGAGCTGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTA 960  
 Db 901 GAGATCTGAGCTGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTA 960  
 961 ATTACAGTGAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1020  
 Db 961 ATTACAGTGAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1020  
 1021 GCTAACCTATGCTGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1080  
 Db 1021 GCTAACCTATGCTGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1080  
 1081 GAAAAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1140  
 Db 1081 GAAAAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1140  
 1141 GCTCAACAGAGACAGCTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1200  
 Db 1141 GCTCAACAGAGACAGCTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1200  
 1201 ACAGCTGAGCAGCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1260  
 Db 1201 ACAGCTGAGCAGCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1260  
 1261 ATTGAAGAAAGTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1320  
 Db 1261 ATTGAAGAAAGTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1320  
 1321 CTTGCTGCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1380  
 Db 1321 CTTGCTGCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1380  
 1381 GTAGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1440  
 Db 1381 GTAGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1440  
 1441 GATGCTGTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1500

Db 1441 GAATGGGTAGATGATGTTACACAGATGATGATGATGATGATGATGATGAT 1500  
 1501 CTTCAAAATGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
 Db 1501 CTTCAAAATGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
 1561 AAACCTGAGCAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1605  
 Db 1561 AAACCTGAGCAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1605

## RESULT 7

ABN71527/c  
ID ABN71527 standard; DNA; 2155561 BP.

ABN71527;  
AC

02-JUL-2002 (first entry)  
XX

Streptococcus polynucleotide SEQ ID NO 10967.  
DE

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW

group A streptococcus; Streptococcus pyogenes; antibacterial; gene;  
KW

antibacterial; infection; vaccine; meningitis; gene therapy; ds.  
XX

Streptococcus sp.  
XX

MO200234771-A2.  
XX

02-MAY-2002.  
XX

29-OCT-2001; 2001MO-GB04789.  
XX

27-OCT-2000; 2000GB-0026333.  
XX

24-NOV-2000; 2000GB-0028727.  
XX

07-MAR-2001; 2001GB-0005640.  
XX

(CHIR-) CHIRON SPA.  
PA

(GENO-) INST GENOMIC RES.  
PA

Tellord J, Masignani V, Margarit Ros Yi, Grandi G, Fraser C;  
PI

Tellord J;  
DR

WPI: 2002-352536/38.  
XX

New Streptococcus protein for the treatment or prevention of infection  
PT

or disease caused by Streptococcus bacteria, such as meningitis, and  
PT

for detecting a compound that binds to the protein.  
XX

Claim 8; Page 4196-4488; 4525pp; English.  
PS

The invention relates to a protein (ABP25413-ABP10895) from group B  
CC

Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC

(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC

the specification. The proteins have antibacterial and anti-inflammatory  
CC

activity. (i), nucleic acids encoding (i), ABN6044-ABN71526 and  
CC

antibodies that bind (i) are used in the manufacture of medicaments for  
CC

Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC

Nucleic acids encoding (i) are used to detect Streptococcus in a  
CC

biological sample. (i) is used to determine whether a compound binds to  
CC

used as a vaccine or diagnostic composition. The disease caused by  
CC

Streptococcus (i) may be used to recombinantly produce (i) and may be  
CC

used in gene therapy. Antibodies to (i) are used for affinity  
CC

chromatography, immunosays, and distinguishing/identifying  
CC

Streptococcus proteins.  
XX

Sequence 2155561 BP; 695741 A; 385320 C; 382958 G; 691542 T; 0 other;  
SQ

Query Match

64.9%; Score 1062.4; DB 24; Length 2155561;



Best Local Similarity 79.2%; Pred. No. 9,8e-267;  
Matches 1274; Conservative 0; Mismatches 331; Indels 3; Gaps 1;

[illegible]

Accession	Gene	Strain	Species	Accession	Gene	Strain	Species	
Db 20232459	GCATATCGGGGTGCTATCATATTAAGTCACAGATGAGAGGCTACAACTTCGTGATTTGATTCGT	20231310	Y1081	GAATAACTACAAAGACGTTTGGGAAATTAAGTCGTGCTGCTGCTATACAAATAGGA	1140	Db 20231389	GAATAATTTACAGAAAGACACTCTCTAAGTATGACCGGTGGTGTAGCAGATATTTAAAGTTGGT	20231310
Y1141	GCCTCACAAGACAGACGCTTTTAAAGAAATGAAACTTCGATTTGAGATGCTCTAAATGCT	1200	Db 20231319	GCAGCAGCTGAAACAGAAATTTAAAGAGATGAACCTTGCATCAGACAGATGCGTAAATGCA	20230700	Y1201	ACACGTGACACCGCTTTGAAGAAGTATCGTCTGCTGCTGCTGAGACGACCTTTATACGGTT	1260
Db 20230659	ACGGGTGCTGCGAGTGTGAAGAGATATGTTTTCAGGTGAGAGGTGAGCGCTCTGTGTAAAGCTT	20230100	Y1261	ATTGAAAAAGTACGACGCTCTTGAGCTTGAGGGCGATGATGCTACTGACGATTAATGTG	1320	Db 20230009	ATTGAAAAAGTACGAGGCGACTGAAACTTAATGCTGATGAGAGAGCTGAGACGTAAATATGTT	20229550
Y1321	CTTCGTGCTCTGAGAAAGACCTGTACGCTCAAAATTCGCTTTAAATGCTGGGTACAGAGGCTCC	1380	Db 2022949	CTTCGTGCTCTGAGAAAGACCTGTACGCTCAAAATTCGCTTTAAATGCTGGGTACAGAGGCTCC	20228900	Y1381	GTAGTATTATGACAAAGTGAAGAAACAGCCCTGACAGAGACAGATTAATGCTGCTACAGAGGT	1440
Db 20228899	GTATATATATTTGAACCTTTTAAACAGCTCGAAATTTGGTACAGAGATTTAAATGCGGCATATGA	20228300	Y1441	GAGTGGGTGATGATGATTTAAACAGAGATTCATTGACCTGCTGCAAGTAAACAGATCAGCG	1500	Db 20228239	GATGTGGTATGATATGTTATGCTACACAGATGATCATTTGACCTGTCAAGATTAACAGCTGTGCGA	20227700
Y1501	CTTCAAAATATGACGCTCTGTAGCTAGTCTTATTTTGAACAGAGAGATGTTGCTTAAT	1560	Db 20227769	CTTCAAAATATGAGGAGATCTGTGACAAAGCTTATCTTGACTACAGACAGATGATGCAAAAT	20227100	Y1561	AAACCTGAAAC---AGCTACGCCAGCGCAGCAATGCGCAGCGATATG	1605
Db 20227709	AAACCTGAAACCAAGACCTCTACAGCTCTCCATGCTCCATGATGATTCATCTATG	2022662						

PT resistant bacterial infections -

XX Claim 16, Page 231, 380pp; English.

XX The present invention relates to nucleic acids (AAH90701-AAH90918)  
XX encoding polypeptides (AAH01002-AAH01114), which are essential for the  
XX viability of a bacterial cell wall. The acronym CFE stands for "Cef For  
XX Expression", where Cef stands for "Conserved Essential Gene". The nucleic  
XX acids are useful for detecting the presence of proteins essential for the  
XX viability of a bacterial cell wall in samples such as cells, tissues,  
XX biological fluids, blood, serum, nose, ear or throat swabs with ligands,  
XX and for detecting corresponding target nucleic acid molecules with  
XX complementary sequences. The nucleic acids are also useful for  
XX determining whether a genomic nucleotide sequence of interest is  
XX essential for viability of a bacterial cell or whether it resides within  
XX an operon, by integrating an exogenous nucleotide sequence comprising a  
XX portion of an open reading frame of the genomic sequence of interest  
XX (comprising 200-500 base pairs) into the genomic sequence of interest  
XX which confers a selectable phenotype to the cell, and determining cell  
XX viability with a selection agent such as chloramphenicol. The nucleic  
XX acids and proteins are also useful as vaccines and for treating bacterial  
XX infections with gene therapy and antisense therapy. The nucleic acids  
XX also enable identification of targets suitable for the treatment of  
XX antibiotic resistant bacterial infections.

XX Sequence 1623 BP; 490 A; 325 C; 394 G; 414 T; 0 other;

Query Match 63.4%; Score 1039.2; DB 22; Length 1623;

Best Local Similarity 77.6%; Pred. No. 6,6e-262;

Matches 1257; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

QY 1 ATGCCAAGAAGAAATCAATTTTCAGCAGATGCGCGCTGCGATGGTGGCGGAGTTGAT 60  
DB 1 ATGCCAAGAAGAAATCAATTTTCAGCAGATGCGCGCTGCGATGGTGGCGGAGTTGAT 60  
QY 61 ATGTAGCAGATACCGTCAAAAGTACGCTGCTTAAGGCGGCAATGTTGTTCTTGAA 120  
DB 61 ATGTAGCAGATACCGTCAAAAGTACGCTGCTTAAGGCGGCAATGTTGTTCTTGAA 120  
QY 121 AAAGCTTTGGTCTCCCTTAATTAAGTAAAGGCGGCAATGTTGTTCTTGAA 180  
DB 121 AAAGCTTTGGTCTCCCTTAATTAAGTAAAGGCGGCAATGTTGTTCTTGAA 180  
QY 122 AATGATTCGCTTCAACCTTGATTAACATGAGGCTGACCAATTCCTTCTTGAA 180  
DB 122 AATGATTCGCTTCAACCTTGATTAACATGAGGCTGACCAATTCCTTCTTGAA 180  
QY 181 TTGGAAGTCAATTTTGAAGATGAGCAAAATTTGCTGTAAGTGGCTTTTAAACC 240  
DB 181 TTGGAAGTCAATTTTGAAGATGAGCAAAATTTGCTGTAAGTGGCTTTTAAACC 240  
QY 241 AATGATTCGCTTCAACCTTGATTAACATGAGGCTGACCAATTCCTTCTTGAA 300  
DB 241 AATGATTCGCTTCAACCTTGATTAACATGAGGCTGACCAATTCCTTCTTGAA 300  
QY 301 GAAGGCTAAAGAAATGTGACAGAGTGTCAATGATGTTCCGTCGAGGATGAA 360  
DB 301 GAAGGCTAAAGAAATGTGACAGAGTGTCAATGATGTTCCGTCGAGGATGAA 360  
QY 361 GAAGGCTAAAGAAATGTGACAGAGTGTCAATGATGTTCCGTCGAGGATGAA 420  
DB 361 GAAGGCTAAAGAAATGTGACAGAGTGTCAATGATGTTCCGTCGAGGATGAA 420  
QY 421 GAAGGCTAAAGAAATGTGACAGAGTGTCAATGATGTTCCGTCGAGGATGAA 480  
DB 421 GAAGGCTAAAGAAATGTGACAGAGTGTCAATGATGTTCCGTCGAGGATGAA 480  
QY 481 TGAGAACCTTGGAGCGTGTGGCAACGATGTTGATACATGCAAGAAATTCGAGGT 540  
DB 481 TGAGAACCTTGGAGCGTGTGGCAACGATGTTGATACATGCAAGAAATTCGAGGT 540  
QY 541 ATGGAACAGAACTGAAGTGTGAAGCATCAATTTGACCGTGTACCTGCTCAA 600  
DB 541 ATGGAACAGAACTGAAGTGTGAAGCATCAATTTGACCGTGTACCTGCTCAA 600  
QY 601 TACATGCTCAGACAAATGAAGAAATGTTGAGAGCTGTAAACCCATTTATCTTAATC 660  
DB 601 TACATGCTCAGACAAATGAAGAAATGTTGAGAGCTGTAAACCCATTTATCTTAATC 660

DB 601 TACATGCTCAGACAAATGAAGAAATGTTGAGAGCTGTAAACCCATTTATCTTAATC 660  
QY 661 ACGGATTAAGAAATGTGCAACATCCCAAGCAATTTGGCACTCTGAGAAATGTTCTAA 720  
DB 661 ACGGATTAAGAAATGTGCAACATCCCAAGCAATTTGGCACTCTGAGAAATGTTCTAA 720  
QY 721 ACCAAGCTGCTATCTCTATTTATGCAATGATGATGATGATGATGATGATGATGATG 780  
DB 721 ACCAAGCTGCTATCTCTATTTATGCAATGATGATGATGATGATGATGATGATGATG 780  
QY 781 GTCTTGAACAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
DB 781 GTCTTGAACAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
QY 841 GATGCTGTAAGCTATGCTGTAAGCAATGCTATCTTGTACAGTGTGATGATGATGATG 900  
DB 841 GATGCTGTAAGCTATGCTGTAAGCAATGCTATCTTGTACAGTGTGATGATGATGATG 900  
QY 901 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
DB 901 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
QY 961 ATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
DB 961 ATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
QY 1021 GCTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080  
DB 1021 GCTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080  
QY 1081 GAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
DB 1081 GAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
QY 1141 GCTGCAACAGACAGCTTTAAAGAAATGAACTTGCATGATGATGATGATGATGATG 1200  
DB 1141 GCTGCAACAGACAGCTTTAAAGAAATGAACTTGCATGATGATGATGATGATGATG 1200  
QY 1201 ACAGCTGACAGCGCTGTAAGAAAGTATCGTGTGCTGCTGCTGCTGCTGCTGCTG 1260  
DB 1201 ACAGCTGACAGCGCTGTAAGAAAGTATCGTGTGCTGCTGCTGCTGCTGCTGCTG 1260  
QY 1261 ATTGAAGAAAGTACAGCTCTTGTGAGGCGGATGATGATGATGATGATGATGATG 1320  
DB 1261 ATTGAAGAAAGTACAGCTCTTGTGAGGCGGATGATGATGATGATGATGATGATG 1320  
QY 1321 CTTCGCTGCTGTAAGAAAGCTGATGATGATGATGATGATGATGATGATGATG 1380  
DB 1321 CTTCGCTGCTGTAAGAAAGCTGATGATGATGATGATGATGATGATGATGATG 1380  
QY 1381 GTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
DB 1381 GTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
QY 1441 GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500  
DB 1441 GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500  
QY 1501 CTTCGCTGCTGTAAGAAAGCTGATGATGATGATGATGATGATGATGATGATG 1560  
DB 1501 CTTCGCTGCTGTAAGAAAGCTGATGATGATGATGATGATGATGATGATGATG 1560  
QY 1561 AAACCTGAAACAGCTACAGGCTGACAGCAATGCCAGGATGATGATGATGATGATG 1620  
DB 1561 AAACCTGAAACAGCTACAGGCTGACAGCAATGCCAGGATGATGATGATGATGATG 1620

RESULT 9  
AAF25036  
ID AAF25036 standard; DNN: 1926 BP.  
XX  
XX AAF25036;  
XX



Db 1321 CTCCTGCTTGGAGAACCTGTCGTAATTCGTCACATGAGATTTGAAGATCT 1380  
 QY 1381 GTAGTTATGACAGTTGAAAAAGACCCCTGACGAAAGATTTAATGTCACACAGT 1440  
 Db 1381 ATGTTATGATGATCTTTGAAAAATCTGAGCTTGATAGATTTCAACGACCAATGCG 1440  
 QY 1441 GAGTGGCTGATGATTAATAACAGGATCATTTGACCTGTCAAAAGTAACAGATCAGCG 1500  
 Db 1441 GAGTGGCTGATGATTAATAACAGGATCATTTGACCTGTCAAAAGTAAGTGAATGTCAGCC 1500  
 QY 1501 CTTCAAAATGACAGCTTCTGACCTAGTCTTATTTGACAAAGAAAGAGTGTGCTGAT 1560  
 Db 1501 CTACAAAATGACAGCTTCTGACCTAGTCTTATTTGACAAAGAAAGAGTGTGCTGAT 1560  
 QY 1561 AATCGTGAACAGCTTCTGACCTAGTCTTATTTGACAAAGAAAGAGTGTGCTGAT 1620  
 Db 1561 AATCGTGAACAGCTTCTGACCTAGTCTTATTTGACAAAGAAAGAGTGTGCTGAT 1620  
 QY 1621 GGTG 1624  
 Db 1621 GGAG 1624

## RESULT 10

AX86153  
 ID AX86153 standard; DNA; 1654 BP.

AX86153:

22-SEP-1999 (first entry)

DNA encoding a Streptococcus pneumoniae heat shock protein (Hsp)60-2.

Heat shock protein; Hsp60-2; Immune response; immunological carrier; cancer control; tumour; sarcoma; cancer; gene therapy; ss.

Streptococcus pneumoniae.

MO9935270-A1.

15-JUL-1999.

29-DEC-1998; 98MO-CA01203.

31-DEC-1997; 97US-0001737.

(STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

Mizzen L, Wisniewski J;

WPI: 1999-430397/36.

P-PSDB: AAY23902.

New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis

Claim 3; Fig 2A-B; 176p; English.

The present sequence encodes a heat shock protein, designated Hsp60-2.  
 The protein, its fragments, variants and fusion proteins, are  
 used to elicit or enhance an immune response against Streptococcus,  
 and to elicit a similar response to a target antigen fused to the  
 protein. Unlike other immunological carriers, Hsp60 proteins are not  
 immunosuppressive so provide an increased response to any conjugated or  
 fused antigen. Also, where used for cancer control, they lack the side  
 effects associated with endotoxins. They can also be used to detect  
 specific antibodies and in treatment or prevention of tumours  
 (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or  
 liver). The Hsp60 polynucleotide is used for recombinant production  
 of the protein, as a source of primers and probes for detecting  
 streptococci in standard hybridization/amplification assays, and  
 therapeutically in gene therapy vectors.

XX  
 SO Sequence 1654 BP; 500 A; 326 C; 401 G; 427 T; 0 other;  
 Query Match 63.4%; Score 1038; DB 20; Length 1654;  
 Best local similarity 77.5%; Pred. No. 1,4e+261;  
 Matches 1257; Conservative 0; Mismatches 363; Indels 0; Gaps 0.

QY 1 ATGGCAAAATCAATTTTACGACATGCGCTGCTCCATGTCGCGAGTGAAT 60  
 Db 15 ATGGCAAAATCAATTTTACGACATGCGCTGCTCCATGTCGCGAGTGAAT 74  
 QY 61 ATGTACAGATACCGTCAAAAGTAACGCTTGCTTAAAGGCGCAATGTTGTTTGA 120  
 Db 75 ATCTTCAAGTACTGTTAAAGTAACCTTGGACCAAAAGTGCATATGTCGTTTGA 134  
 QY 121 AAAGCTTTGCTTCCCTTAATTAATATACGAGGGAATACCATTCGTAAGATCGAA 180  
 Db 135 AAGTCATTCGCTTCACTTGAATTAACCAATGCGGTGCTATTCGCAAAAGATTA 194  
 QY 181 TTAGAGATCATTTTGAAGACATGGAGCAAAATGGTGTGTAAGTGGCTGTAAGC 240  
 Db 195 TTAGAGATCATTTTGAAGACATGGAGCAAAATGGTGTGTAAGTGGCTGTAAGC 254  
 QY 241 AATGATATGCTGTGATGGAGACTACTGCAAGTATTTGACAAAGCATGTCAT 300  
 Db 255 AATGATATGCTGTGATGGAGACTACTGCAAGTATTTGACAAAGCATGTCAT 314  
 QY 301 GAAGACTAAATAATGTGACAGAGGTGCTAATGCAATTTGATCCGTGAGCATGAA 360  
 Db 315 GAAGACTAAATAATGTGACAGAGGTGCTAATGCAATTTGATCCGTGAGCATGAA 374  
 QY 361 ACACGACAGCAACAGCTGTTGAAGCTTTGAAGCCATGCTCAACCTGATCTGCAAG 420  
 Db 375 ACACGACAGCAACAGCTGTTGAAGCTTTGAAGCCATGCTGATCTGCAAG 434  
 QY 421 GAAGCTATTTGCTCAAGTCTGCAATCATCAGCTCTGAAAAGTTGGAGATATTC 480  
 Db 435 GAAGCTATTTGCTCAAGTCTGCAATCATCAGCTCTGAAAAGTTGGAGATATTC 494  
 QY 481 TCAGAACATATGAGCGTGTGGCAACAGATGTGATTAATCAATCGAAGATCTGAGT 540  
 Db 495 TCAGAACATATGAGCGTGTGGCAACAGATGTGATTAATCAATCGAAGATCTGAGT 554  
 QY 541 ATGGAACAGACTGAAGTGTGGAAGCATGATTTGACCGGTTCACGCTCAA 600  
 Db 555 ATGGAACAGACTGAAGTGTGGAAGCATGATTTGACCGGTTCACGCTCAA 614  
 QY 601 TACATGTCACAGACATGAAAAATGTTGACAGCTTGAAAAACCATTTATCTTAATC 660  
 Db 615 TACATGTCACAGACATGAAAAATGTTGACAGCTTGAAAAACCATTTATCTTAATC 674  
 QY 661 ACGGATAAAAAGTGTCAAAACATCCAGACATTTTGCACACTGTAAGGAAGTTCTAAA 720  
 Db 675 ACGGATAAAAAGTGTCAAAACATCCAGACATTTTGCACACTGTAAGGAAGTTCTAAA 734  
 QY 721 ACGAAGCTCATATCATATATTCAGATGATGTGATGAGACACTTCAACCTT 780  
 Db 735 ACGAAGCTCATATCATATATTCAGATGATGTGATGAGACACTTCAACCTT 794  
 QY 781 GCTGTGAACAATTCGTGTGACTTTCAATGTGTTGCTGCAAGGCGCAGAGATTTG 840  
 Db 795 GCTGTGTGAACAATTCGTGTGACTTTCAATGTGTTGCTGCAAGGCGCAGAGATTTG 854  
 QY 841 GATCGCTGAAGCTATGCTGTAACATTTGCTATTTGACAGGTGTACAGTATTA 900  
 Db 855 GATCGCTGAAGCTATGCTGTAACATTTGCTATTTGACAGGTGTACAGTATTA 914  
 QY 901 GAGATCTGAGCTGAATTAAGATCTCAATGACAGCCTTGGACAGGCTGCTTAAG 960  
 Db 915 GAGATCTGAGCTGAATTAAGATCTCAATGACAGCCTTGGACAGGCTGCTTAAG 974  
 QY 961 ATTACAGTTGAATAAGATACAGACTAATGTTGAAGTTCAGGAGTTCAGAGATATT 1020



RESULT 12  
 AAH56860  
 ID AAH56860 standard; DNA: 2107 BP.  
 AC AAH56860:  
 DT 06-SEP-2001 (first entry)  
 DE Antibiotic resistant *S. pneumoniae* groE operon sequence SEQ ID NO:6.  
 XX  
 XX Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;  
 KM microorganism; *Escherichia coli*; *Streptococcus pneumoniae*; diagnosis;  
 KM *Streptococcus pyogenes*; *Staphylococcus aureus*; *Pseudomonas aeruginosa*;  
 KM antibacterial; antiviral; antiproliferative; antisense therapy;  
 KM microbial infection; ds.  
 XX  
 OS *Streptococcus pneumoniae*.  
 XX  
 PN WO200136625-A2.  
 XX  
 XX 25-MAY-2001.  
 PD  
 PD 20-NOV-2000; 2000MO-CA01347.  
 PF  
 PF 18-NOV-1999; 99US-0166249.  
 XX  
 XX (GENE-) GENESENSE TECHNOLOGIES INC.  
 PA  
 PA Wright JA, Young AH, Dugourd D;  
 PI  
 PI WPI: 2001-355633/37.  
 DR  
 DR  
 XX  
 XX Novel antisense compounds targeting nucleic acid encoding groEL or  
 PT groES gene of microorganism, which hybridize with and inhibit  
 PT expression of the genes, useful to inhibit growth of microorganism  
 PT having the genes -  
 XX  
 PS Disclosure: Fig 6; 110PP; English.  
 XX  
 XX The present invention specifically claims AAH56366 to AAH56832 which are  
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More  
 CC generally, antisense compounds (I) comprising antisense oligonucleotides  
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat  
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a  
 CC microorganism, where the antisense compound is complementary to GL or  
 CC GS of a microorganism and specifically hybridizes with and inhibits the  
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral  
 CC and antiproliferative activities, and can be used in antisense therapy  
 CC and for inhibition of expression of groES or groEL. (I) are useful for  
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are  
 CC also useful for inhibiting the growth of a microorganism, or inhibiting  
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or  
 CC a virus) having a GL or GS gene which involves administering to the  
 CC microorganism or to a cell infected with the microorganism, (I) are  
 CC also useful for treating a mammalian pathological condition mediated by  
 CC the microorganisms which involves identifying a eukaryotic organism  
 CC having a pathological condition mediated by microorganisms having a GL  
 CC or GS gene and administering (I) such that the growth of microorganism  
 CC is inhibited. The antisense compounds are utilized for diagnostics,  
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to  
 CC prevent or delay microbial infections in humans. They are also useful as  
 CC molecular weight markers. AAH56367 to AAH56367 and AAH56633 to AAH56854  
 CC represent PCR primers for groE sequences which are used in the  
 CC amplification of the present invention. AAH56855 to AAH56870 represent  
 CC groE nucleotide sequence given in the present invention.  
 XX  
 XX Sequence 2107 BP: 650 A; 400 C; 508 G; 549 T; 0 other;  
 QX  
 Query Match 63.2%; Score 1036; DB 22; Length 2107;  
 Best Local Similarity 77.5%; Pred. No. 5e-261;  
 Matches 1255; Conservative 0; Mismatches 365; Indels 0; Gaps 0

OY 1 ATGCCAAGAAATCAATTTTCAGCAGATGCGCGTCTCCATGATGCGGAGTTGAT 60  
 DB 485 ATGTCAAAAGAAATTAATTTTCATCAGATGCGCGTTCACATATGTCGGTGTGCGAT 544  
 OY 61 ATGTACAGATATGCGTCAAGTAAAGCTGCTTAAAGGCGCAATGTTGTTGGA 120  
 DB 545 ATCCGTGCAGATATGTTAAAGTAACTTGGACCAACATGCGTGTCTTGA 604  
 OY 121 AAGCTTGTGCTCCCTTAATTAATGCGGGTAACCATGCTTAAGATCGAA 180  
 DB 605 AATTCATTTGGCTCACCATTTATACCATGACGCTGTGCAATGTCGCAAGAAATGGA 664  
 OY 181 TTAAGAAATATTTGAAACATGGAGCAAAATGCTGTGGAAGTGGCTTTAAACC 240  
 DB 665 TTAGAGACATTTTGAATAATGGTCAAAATGATATGCAAGAAATGCTTTAAACC 724  
 OY 241 AATGATATGCTGTGTATGAGCACTACTCAACAGTTTGAACAAGCATTTTCAT 300  
 DB 725 AATGATATGCTGTGTATGAGCACTACTCAACAGCATTTTCATGCAAGCATGTCGCT 784  
 OY 301 GAAGCACTAAATAATGTGACAGAGTGTATCAATTTGATGCTGCGTCAAGCATTTGA 360  
 DB 785 GAAGCACTAAATAATGTGACAGAGTGTATCAATTTGATGCTGCGTCAAGCATTTGA 844  
 OY 361 ACAGCAAGCAAGCAAGCTGTGGAAGCTTGAAGCATTTGCTCAAGCATTTGCTCAAG 420  
 DB 845 ACAGCAAGCTGTGCGAGCAAGCTGTGGAAGCATTTGCTCAAGCATTTGCTCAAGCATTTGA 904  
 OY 421 GAAGCACTGTGCTGAGCTGCTGAGATATCAACCTGCTGAAAGATGAGATATTC 480  
 DB 905 GAAGCACTGTGCTGAGCTGCTGAGATATCAACCTGCTGAAAGATGAGATATTC 964  
 OY 481 TCAAGCACTGAGAGCTGTGGCAACAGATGTGTATTCATCGAAGATATCGAGT 540  
 DB 965 TCAAGCACTGAGAGCTGTGGCAACAGATGTGTATTCATCGAAGATATCGAGT 1024  
 OY 541 ATGGAACAGAACTTGAAGTGTGAAGCAATTTGACAGCTGTGCTGCTCA 600  
 DB 1025 ATGGAACAGAACTTGAAGTGTGAAGCAATTTGACAGCTGTGCTGCTCA 1084  
 OY 601 TACATGCTACAGCAATGAAATAATGCTTGCAGACCTTGAAGCATTTATCTATC 660  
 DB 1085 TACATGCTACAGCAATGAAATAATGCTTGCAGACCTTGAAGCATTTATCTATC 1144  
 OY 661 ACGGATTAATAAGTGTCAAAATCCAAATCTTCCGCACTGTGAGAAATGCTTAA 720  
 DB 1145 ACGGATTAATAAGTGTCAAAATCTTCCGCACTGTGAGAAATGCTTAA 1204  
 OY 721 ACGGATTAATAAGTGTCAAAATCTTCCGCACTGTGAGAAATGCTTAA 780  
 DB 1205 ACGGATTAATAAGTGTCAAAATCTTCCGCACTGTGAGAAATGCTTAA 1264  
 OY 781 GTCGTAACAGATTTGCTGCTCAATGCTGTGCTCAAGGCGCATTTGCT 840  
 DB 1265 GTCGTAACAGATTTGCTGCTCAATGCTGTGCTCAAGGCGCATTTGCT 1324  
 OY 841 GATGCTGTAAGCTATGCTGAAGCAATTTGCTGCTCAAGGCGCATTTGCT 900  
 DB 1325 GATGCTGTAAGCTATGCTGAAGCAATTTGCTGCTCAAGGCGCATTTGCT 1384  
 OY 901 GAGGATCTAGGCTTGAATTAAGATCTCAATGCTGCTGAGGCTGTGAGGCTCTAG 960  
 DB 1385 GAGGATCTAGGCTTGAATTAAGATCTCAATGCTGCTGAGGCTGTGAGGCTCTAG 1444  
 OY 961 ATTACAGTGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020  
 DB 1445 ATTACAGTGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1504  
 OY 1021 GCTAACGCTATGCTGATTAATGCAATTTGAAGCAACACTTGTGATGCTGCT 1080  
 DB 1505 TCTACCGCTGCTGCTGATTAATGCAATTTGAAGCAACACTTGTGATGCTGCT 1564  
 OY 1081 GAAAGCACTGAAGCTTTGCGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140

DB 1565 GAAAGTGAAGCAAGCTTTGGCAAAATTTGCAAGGCTGTGAGGCTTTAAAGTGGGA 1624  
 OY 1141 GCTCAAGAGAGACGCTTTAAAGAAATGAATTCCTGATGAGATGCTTTAAAGCT 1200  
 DB 1625 GCGGCACTGAAGATGAGTGAAGAAATGAATTCCTGATGAGATGCTTTAAAGCT 1684  
 OY 1201 ACAGTGAAGCGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAGACTTTAGAGGT 1260  
 DB 1685 ACTGTAAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAGACTTTAGAGGT 1744  
 OY 1261 ATTGAAGAGTGAAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAGACTTTAG 1320  
 DB 1745 ATTGAAGAGTGAAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAGACTTTAG 1804  
 OY 1321 CTTCAGTGTGAAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAGACTTTAG 1380  
 DB 1805 CTTCAGTGTGAAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAGACTTTAG 1864  
 OY 1381 GATGATATGCAAGTGAAGAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAG 1440  
 DB 1865 GATGATATGCAAGTGAAGAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAG 1924  
 OY 1441 GATGATATGCAAGTGAAGAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAG 1500  
 DB 1925 GATGATATGCAAGTGAAGAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAG 1984  
 OY 1501 CTTCAGTGTGAAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAGACTTTAG 1560  
 DB 1985 CTTCAGTGTGAAGAGCTTGAAGAGATGATGCTGCTGTGAGTGAAGAGACTTTAG 2044  
 OY 1561 AAGCTGAAGCACTGAGCGGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620  
 DB 2045 AAGCTGAAGCACTGAGCGGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2104

## RESULT 13

AAWS2210  
 ID AAWS2210 standard; DNA: 5365 BP.

XX AC AAWS2210;  
 DT 23-OCT-1998 (first entry)  
 XX DE Streptococcus pneumoniae genome fragment SEQ ID NO:77.  
 XX KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;  
 XX KM computer; readable medium; vaccine; pharmaceutical composition; de.  
 XX OS Streptococcus pneumoniae.  
 PN W09818931-A2.  
 PD 07-MAY-1998.  
 PF 30-OCT-1997; 97MO-US19588.  
 PR 31-OCT-1996; 96US-0029960.  
 RA (HUMA-) HUMAN GENOME SCI INC.  
 PI Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;  
 PT Kunsch CA, Rosen CA;  
 DR WPI: 1998-272225/24.  
 XX Computer-readable medium with recorded Streptococcus pneumoniae  
 PT polynucleotide sequences - useful in diagnostic kits and assays, and  
 PT pharmaceutical compositions and vaccines for Streptococcus  
 XX pneumoniae  
 PS Claim 1; Page 628-631; 1409pp; English.



CC The present invention describes a computer readable medium which has  
 CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)  
 CC recorded on it, or a representative fragment or a sequence at least 95%  
 CC identical to SEQ ID NO:1 to 391. The nucleotide sequences depicted in  
 CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from  
 CC *Streptococcus pneumoniae*. The present invention also describes a  
 CC isolated nucleic acid molecule encoding a homologue of any of the  
 CC fragments of the *S. pneumoniae* genome (SEQ ID NO:1 to 391) where the  
 CC nucleic acid molecule is produced by a process comprising: (a) screening  
 CC a genomic DNA library using as a probe a target sequence defined by any  
 CC of the sequences in SEQ ID NO:1 to 391, identifying members of the  
 CC library which contain sequences that hybridize to the target sequence and  
 CC isolating the nucleic acid molecules from the members; or (b) isolating  
 CC mRNA, DNA or cDNA produced from an organism amplifying nucleic acid  
 CC molecules whose nucleotide sequence is homologous to amplification  
 CC primers derived from the fragment of the *S. pneumoniae* genome to prime  
 CC the amplification and isolating the amplified sequences. The computer  
 CC readable medium can be used in a computer-based system for identifying  
 CC fragments of the *S. pneumoniae* genome of commercial importance, or  
 CC expression modulating fragments of the *S. pneumoniae* genome. Products  
 CC from the present invention can be used in diagnosis kits and assays, and  
 CC pharmaceutical compositions and vaccines for *S. pneumoniae*.

XX Sequence 5365 BP; 1654 A; 960 C; 1082 G; 1669 T; 0 other;

Query Match 63.2%; Score 1034.4; DB 19; Length 5365;  
 Best Local Similarity 77.4%; Pred. No. 1.9e-260;

Matches 1254; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

CC 1 ATGCGAAGAAGAAATCAATTTTCACAGATGCGCGTGCATGATGCGCGAGTTGAT 60  
 CC 278 ATGTCAAAAGAAATTAATTTTCATCATGATGCCCGCATGATGATGATGAT 337  
 CC 61 ATGTAGCAGATACCGTCAAGATGCGTGGTCCCAAGAGCGCAATGTTCTTGA 120  
 CC 338 ATCCCTGCGAGCACTGTAAAGTAACTGTGGACCAAAAGTCCCAATGCTTTGAA 397  
 CC 121 AAGCTTTTGTCTCCCTTAATTAATGAGGGGTAACCATTTGTAAGATCGAA 180  
 CC 398 AAGTCATTCGTTACCTTGGTACCATGAGGAGGATGACCATGCAAAATATGAA 457  
 CC 181 TTAGAAGATCTTTTGAAGATGAGGACAAATTTGTGTGTAAGTGGCTTAAACC 240  
 CC 458 TTGGAAGACATTTTGAAGATGAGGAGTAAAGTAAAGTAAAGTAAAGTAAAG 517  
 CC 241 AATGATATGCTGATGATGAGGACACTCAAGATTTTGAACAGCATTTGAT 300  
 CC 518 AATGATATGCGAGTACAGGATACAGATGCAAGATCTTACCAACCTATGTCGT 577  
 CC 301 GAAGACTTAAATATGAGCAGGATGATCAATGATGATGATGATGATGATGAT 360  
 CC 578 GAAGATATCAAAATGATGAGGATGATGATGATGATGATGATGATGATGAT 637  
 CC 361 ACAGCAACAGCAAGCTGTTGAAGCTTGAAGCAATGATGATGATGATGATGAT 420  
 CC 638 ACAGCAAGTGGCCGACCAATGATGATGATGATGATGATGATGATGATGAT 697  
 CC 421 GAAGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 CC 698 GAAGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 757  
 CC 481 TCAGAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
 CC 758 TCTGAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 817  
 CC 541 ATGAAGCAAGCAAGCTGATGATGATGATGATGATGATGATGATGATGAT 600  
 CC 818 ATGAAGCAAGCAAGCTGATGATGATGATGATGATGATGATGATGATGAT 877  
 CC 601 TACATGCTACAGCAATGATGATGATGATGATGATGATGATGATGATGAT 660  
 CC 878 TACATGCTACAGCAATGATGATGATGATGATGATGATGATGATGATGAT 937

CC 661 ACAGATTAAGAAAGTTCACAAAGCAATGATGATGATGATGATGATGATGAT 720  
 CC 938 ACAGCAAGAAATTTCCAAATGATGATGATGATGATGATGATGATGATGAT 997  
 CC 721 ACCAGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 CC 998 ACAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1057  
 CC 781 GCTTGAACAAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 840  
 CC 1058 GTTGTGAACAAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1117  
 CC 841 GATCGCTGAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 900  
 CC 1118 GACCTGCGCAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 1177  
 CC 901 GAGATCTAGCACTGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 CC 1178 GAAGACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1237  
 CC 961 ATTACAGTGAATGAAGATGATGATGATGATGATGATGATGATGATGAT 1020  
 CC 1238 GTGACCTGCGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 1297  
 CC 1021 GCTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
 CC 1298 TCTCAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1357  
 CC 1081 GAAATATCAAGAAAGTGTGATGATGATGATGATGATGATGATGATGAT 1140  
 CC 1358 GAAATATCAAGAAAGTGTGATGATGATGATGATGATGATGATGATGAT 1417  
 CC 1141 GCTCAACAGACAGCTTTAAAGAAATGAAATGAAATGAAATGAAATGAAAT 1200  
 CC 1418 GCGCAACAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1477  
 CC 1201 ACAGCTGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1260  
 CC 1478 ACTGCTGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1337  
 CC 1261 ATTGAAGAAAGTGAAGCTGATGATGATGATGATGATGATGATGATGAT 1320  
 CC 1538 ATTCAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1397  
 CC 1321 CTGCGCTGCTGAAGAGCTGATGATGATGATGATGATGATGATGATGAT 1380  
 CC 1539 CTGCGCTGCTGAAGAGCTGATGATGATGATGATGATGATGATGATGAT 1440  
 CC 1381 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
 CC 1658 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
 CC 1441 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
 CC 1718 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1777  
 CC 1501 CTTCAAATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
 CC 1778 CTACAAATGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1837  
 CC 1561 AAACCTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
 CC 1838 AAACCTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1897

RESULT 14  
 AAH56859  
 ID AAH56859 standard; DNA: 2401 BP.  
 AC AAH56859;  
 XX  
 DT 06-SEP-2001 (first entry)  
 XX



DB 1819 ACTCGTCAGCTGTTGAGAAAGATATTGTCAGTGTGTGACACAGCTCTTCCAAATGTG 1878  
OY 1261 ATTGAAAAAGTAGCAGCTCTGACCTTGAGGCGCATGATGCTAGTACGATGAACTGTGTG 1120  
DB 1879 ATTCCAGCTGAGAGCTACCTTGGAATGACAGAGATGAACACAGACAGTAAATGTGT 1938  
OY 1321 CTTCGCTCTAGAAAGAGCTGTACGTAATGCTTAAATGCTGGAGACAAAGCTCC 1380  
DB 1939 CTCCTGCTTGGAAAGACCGTGTGCAATATGCTCAACATGACAGATTTAAAGATCT 1998  
OY 1381 GTAGTTATGACAGTTGAAAGACCGCTGCAAGAAAGATGATTTAAATGCTCAACAGCT 1440  
DB 1999 ATGCTTATGATGCTTTGAAAAATGCTGACCTGTGATAGATTTAAAGCAGCAACGTGCG 2058  
OY 1441 GAGTGGTGTATGATGATTAAGAAAGATGATGACCTGTCAAGTAAACAGATCAGCG 1500  
DB 2059 GAGTGGTGTATGATGATTAAGAAAGATGATGACCTGTCAAGTAAAGTGTGTCAGCG 2118  
OY 1501 CTTCAAATGACAGCTCTGCTGACGTAATGCTTATTTGACACAGAGAGCTTGTCTAAT 1560  
DB 2119 CTCACAAATGACAGCTCTGCTGACGTAATGCTTATTTGACACAGAGAGCTTGTCTAAT 2178  
OY 1561 AAGCTGAACAGCTCTGACGCAAGCGCAATGCGACAGATGATGATCAGAGATGATG 1620  
DB 2179 AAGCTGAACAGCTCTGACGCAAGCGCAATGCGACAGATGATGATGATGATGATGATG 2238

## RESULT 15

ABA90521 ABA90521 standard; DNA: 2365589 BP.

AC ABA90521;

DT 16-MAY-2002 (first entry)

DE Genomic sequence of *Lactococcus lactis* IL1403.

KM Biotynthesis; biodegradation; lactic bacterium; yogurt; cheese; ds.

OS *Lactococcus lactis* IL1403.

PN FR2807446-A1.

PD 12-OCT-2001.

PE 11-APR-2000; 2000FR-0004630.

PR 11-APR-2000; 2000FR-0004630.

PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

PI Bolotline A, Sorokline A, Renault P, Ehrlich SD;

DR WPI: 2002-043418/06.

XX New nucleotide sequence useful in the identification of *Lactococcus*

PS lactic and related species -

XX Claim 1; SEQ ID 1: 2504bp; French.

CC The present invention is related to a *Lactococcus lactis* nucleotide

CC sequence (ABA90521) and related proteins (AB53300-AB53621). The

CC nucleic acid sequence is useful in the detection and/or amplification of

CC related species. The proteins of the invention are useful for the

CC biosynthesis or biodegradation of a composition of interest. The

CC invention helps research in lactic bacteria, particularly useful in the

CC production of yogurt and cheese.

CC Note: The sequence data for this patent is based on equivalent patent

CC WO2001/7734 (published 18-OCT-2001) which is available in electronic

CC format directly from WIPO at [ftp.wipo.int/pub/published\\_pat\\_sequences](http://ftp.wipo.int/pub/published_pat_sequences).

Query Match 58.38; Score 954.2; DB 24; Length 2365589;  
Best Local Similarity 75.28; Pred. No. 2,2e-238;  
Matches 1190; Conservative 0; Mismatches 393; Indels 0; Gaps 0;

OY 1 ATGCAAAAGAAATCAAAATTTTACAGAGATCGCGCTGCTGACGCTGAGCGGAGTAT 60  
DB 398897 ATGCAAAAGAAATCAAAATTTTACAGAGATCGCGCTGAGAACGAGATAGCGTGAATAT 398956  
OY 61 ATGTACAGATACCGCTCAAGTAAGTACGCTGCTTAAAGGCGCAATGTTGCTGAA 120  
DB 398957 ATGTCTGCTGATACAGTAAACCAACCCCTGACCAAAAGTGTGATGTTGCTGAA 399016  
OY 121 AAAGCTTGTGCTTCCCTTAATTAATGAGAGGAGTAAAGATGATGAA 180  
DB 399017 AAATCATATGATGATCACTTTAATTAACAAACGATGCTTACGATTCGCAAGATGAA 399076  
OY 181 TTAGAAATCATTTTGAAGAAATGAGAGCAAAATGCTGTCAAGCTTCTAAACC 240  
DB 399077 CTGAGATCATTTTGAAGAAATGAGAGCACTTAACTTGTTCAGAGATGCTCAAAAGCA 399136  
OY 241 AATGATATGCTGATGATGATGAGAGACGCTGCAACAGTTTGAACAGCAAGCTTGTAT 300  
DB 399137 AATGATATGCTGATGATGATGAGAGACGCTGCAACAGTTTGAACAGCAAGCTTGTAT 399196  
OY 301 GAGAGACTTAAATTAATGACAGAGCTGCTAATTCATTTGCTATCCGTGAGGACATTTGAA 360  
DB 399197 GAGAGACTTAAATTAATGACAGAGCTGCTAATTCATTTGCTATCCGTGAGGATTTGAA 399256  
OY 361 ACAGCAACAGCAAGCTGTTGAAACCTTGAAGCCATGCTCAACCTGTATCTGCAAG 420  
DB 399257 CTGCTGCTGAAACAGCTGCTGCTGCTGCTAATTAAGAGATGCAATTCCTGTCAGATTA 399316  
OY 421 GAGCTATTGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 399317 TCAGCAATTCGCGCAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399376  
OY 481 TCAGCAATTCGCGCAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
DB 399377 TCTGATGCAATGCAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399436  
OY 541 ATGGAACAGCACTTGAAGTGTGAGAGATGCAATTTGACCGTGTACCTGCTGCA 600  
DB 399437 ATGGAACAGCACTTGAAGTGTGAGAGATGCAATTTGACCGTGTACCTGCTGCA 399496  
OY 601 TACATGCTACAGCAATGAAAAATGCTGCAACCTGGAACCCATTTACTTATC 660  
DB 399497 TATATGCTTCTAATACAGAAAAATGCTGCAATTTGCAATTTACTTATC 399556  
OY 661 ACGGATAAAAAGTGTCAACATCCAGACATTTGCGCACTGTGAGAGATTTTAA 720  
DB 399557 ACGGATAAAAAGTGTCAACATTTGCGCACTGTGAGAGATTTTAA 399616  
OY 721 ACCAAGCTCCATTTACTTATTTGCAAGATGATGATGATGATGATGATGATGATGATGAT 780  
DB 399617 ACCAAGCTCCATTTACTTATTTGCAAGATGATGATGATGATGATGATGATGATGAT 399676  
OY 781 GTCTTGAACAGATGCTGCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
DB 399677 GTCTTGAACAGATGCTGCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399736  
OY 841 GATCGCTGAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
DB 399737 GATCGCTGAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399796  
OY 901 GAGGATCTAGAGCTTAAATTAAGATGCTCAACAGCCCTGAGAGCTGCTGAA 960  
DB 399797 GAGGATCTAGAGCTTAAATTAAGATGCTCAACAGCCCTGAGAGCTGCTGAA 399856  
OY 961 ATTACAGTGAATTAAGATGCAAGTAAATGTTGAAGTTCAGAGATTTGCAAGCTTAT 1020  
DB 399857 GCAACTGTGATTAAGACACACACACAAATTTGTTGAAGTGTGCTGCTGCTGCTGCTGCT 399916

